

Supplemental files for:

Dynamic organization of lncRNA and circular RNA regulators collectively controlled cardiac differentiation in humans

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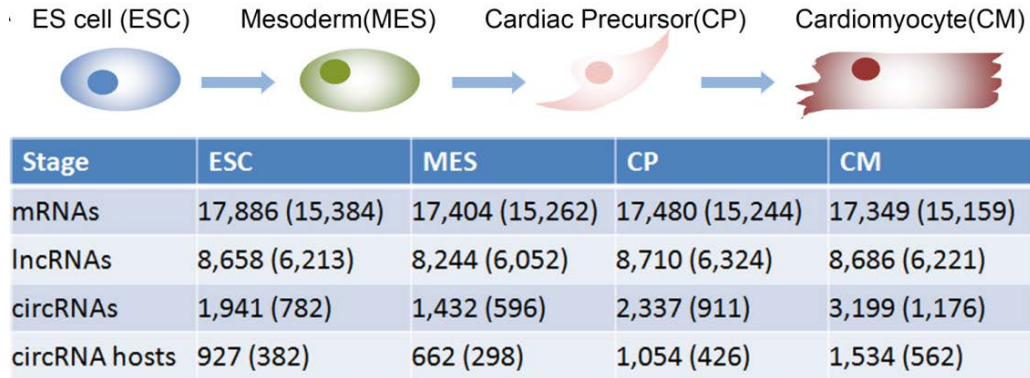


Figure S1. The number of expressed genes during heart differentiation. The digits enclosed represents the genes processed to be used in following analyses.

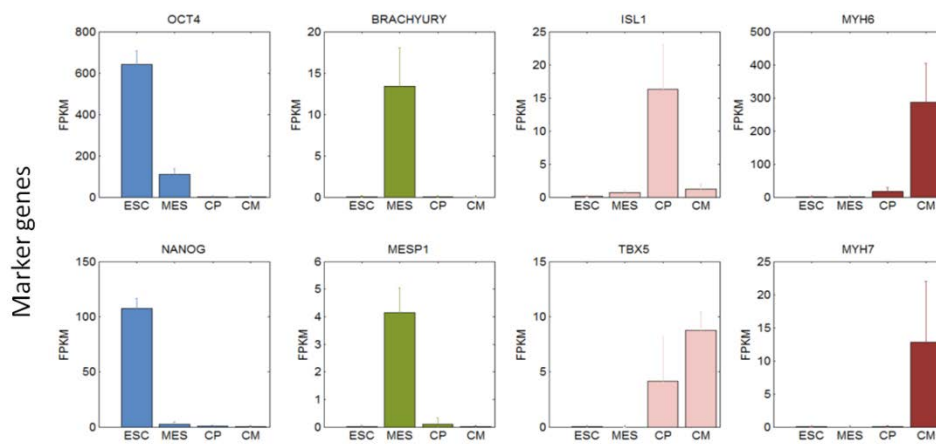


Figure S2. The expression levels of marker genes during heart differentiation.

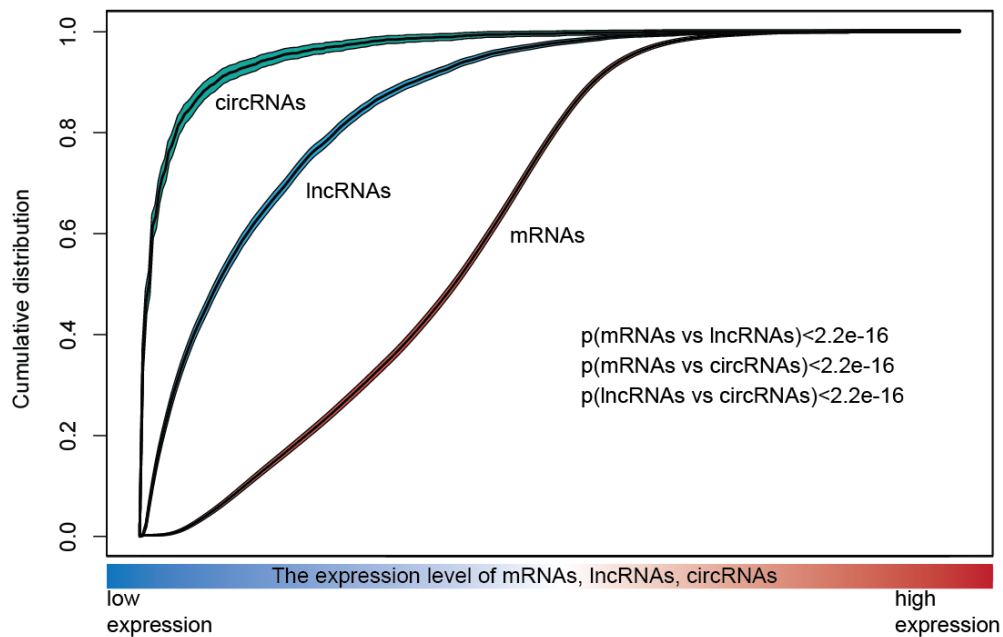


Figure S3. The cumulative distribution of expression of mRNAs, lncRNAs and circRNAs.

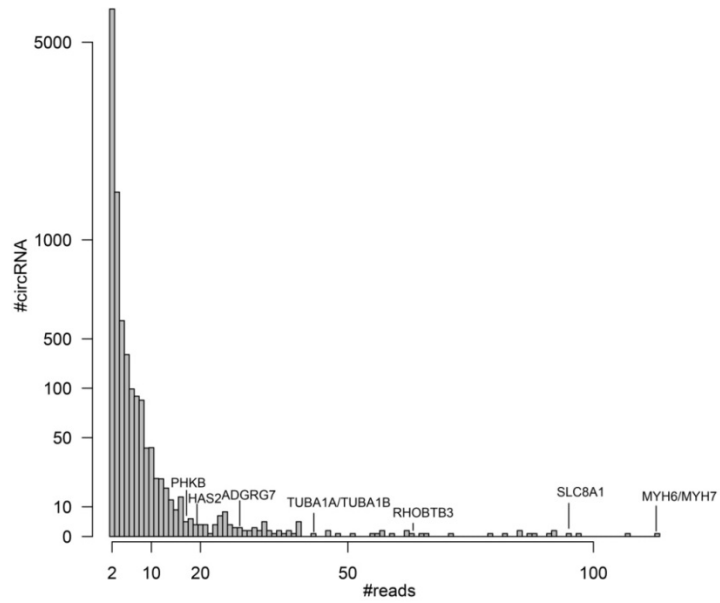


Figure S4. CircRNA expression in cardiac development. The majority of circRNAs were with low abundance but a subset with higher expression.

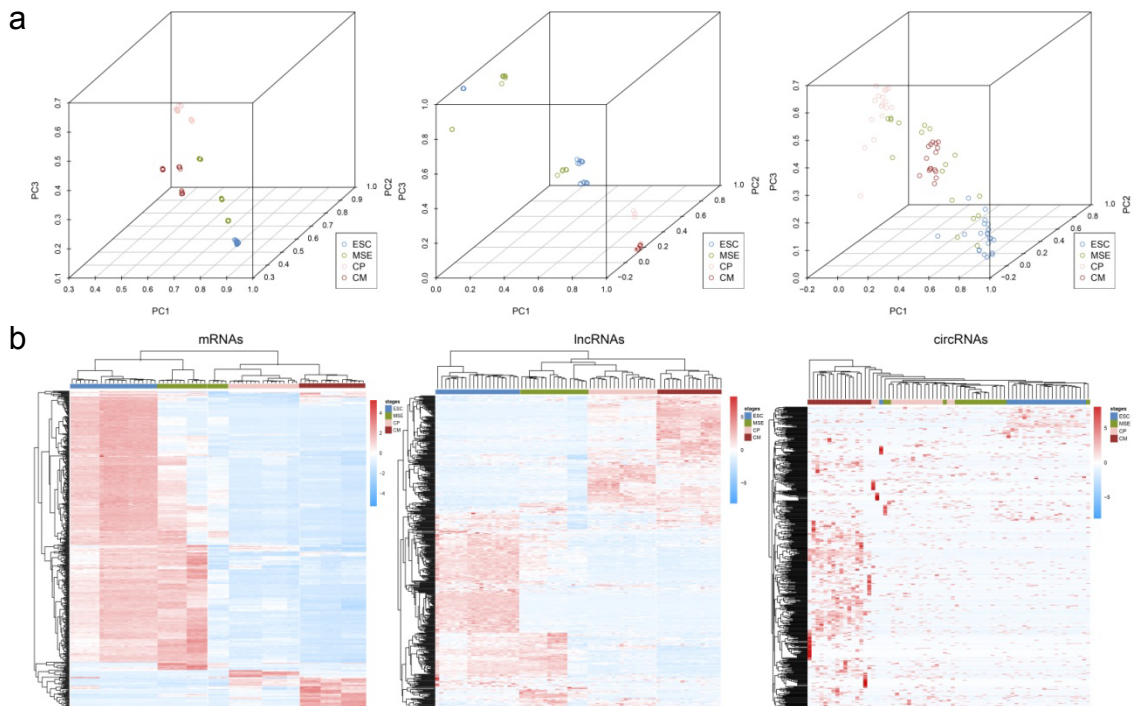


Figure S5. The divergence of samples from distinct cardiac development stages. (a) Principle component analysis of transcriptome in a 3D graph of PC1, PC2 and PC3. The samples in the same stage tend to be grouped together. (b) The hierarchical clustering of top 500 genes, lncRNAs and circRNAs with higher expression variation, showed an apparent stage-specific structure during cardiac development.

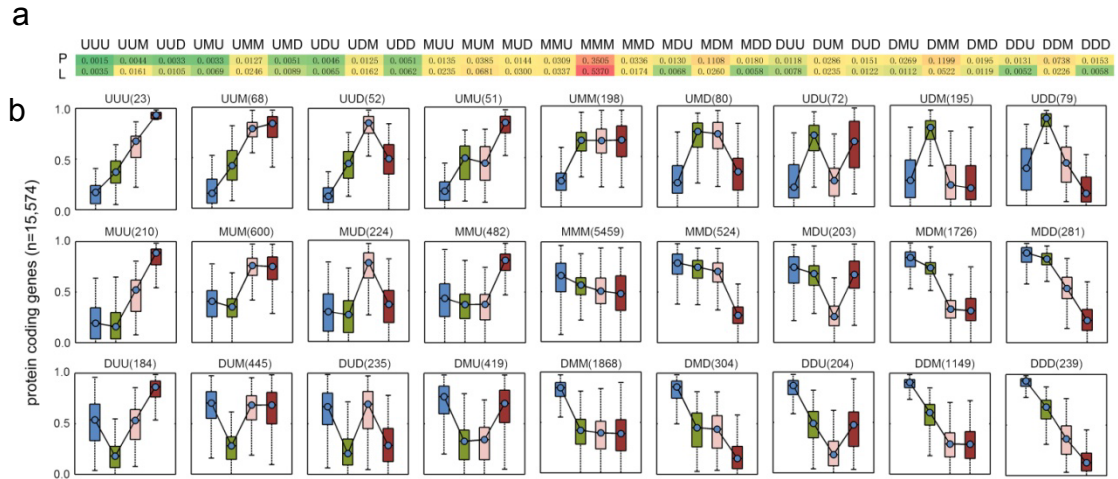


Figure S6. The expression patterns of genes. (a) The percentage of genes (P) and lncRNAs (L) within each pattern. The digits in the table are colored; red indicates a higher proportion and green represents a relatively small percentage. (b) The expression patterns of genes.

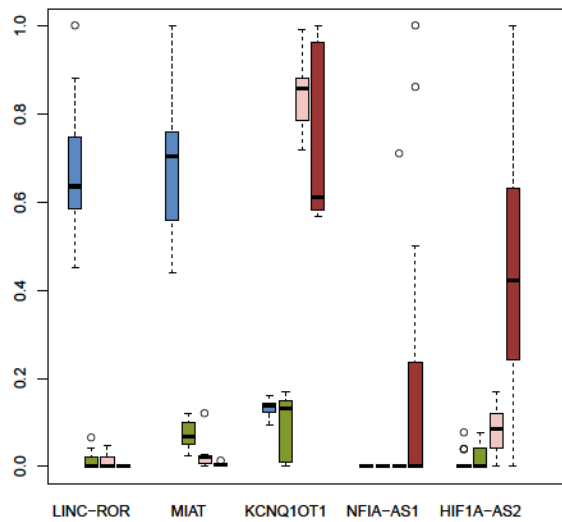


Figure S7. The expression of representative lncRNAs during cardiac differentiation.

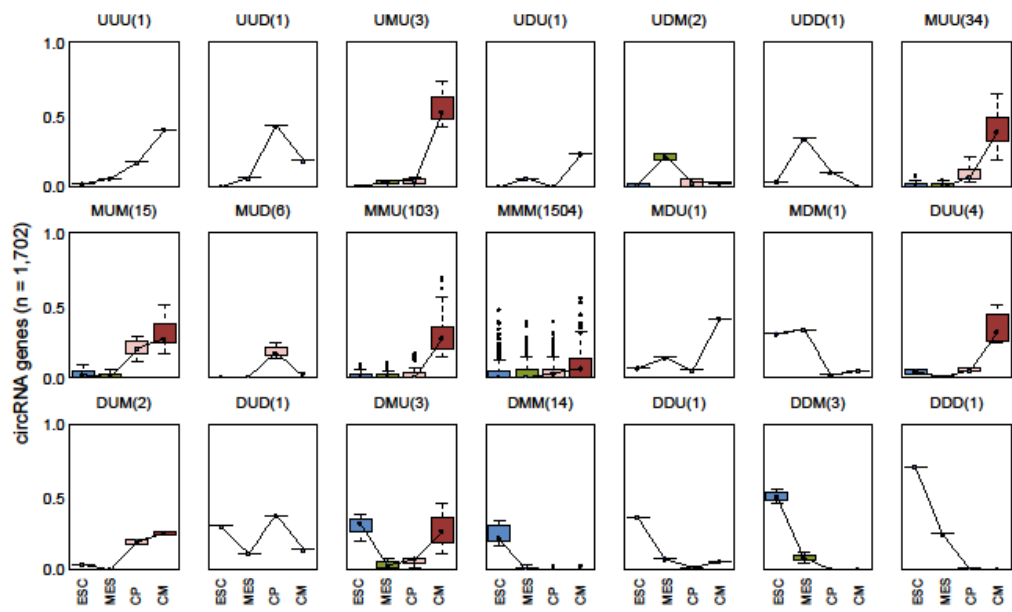


Figure S8. The expression patterns of circRNAs.

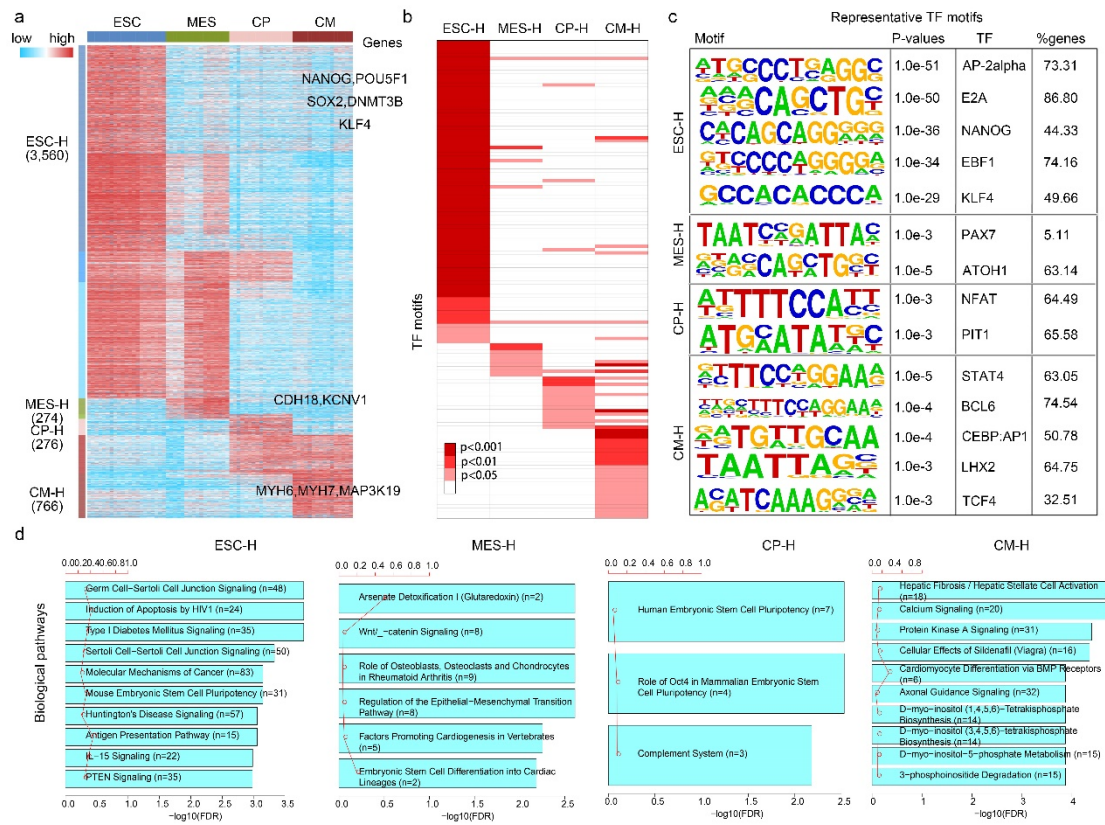


Figure S9. Stage-specific regulations and cellular functions of genes during cardiac differentiation. (a) Dynamic expression profile of genes. (b) Stage-specific enrichment of TF motifs. (c) Some representative TF motifs. (d) Biological processes enriched by stage-specific genes.

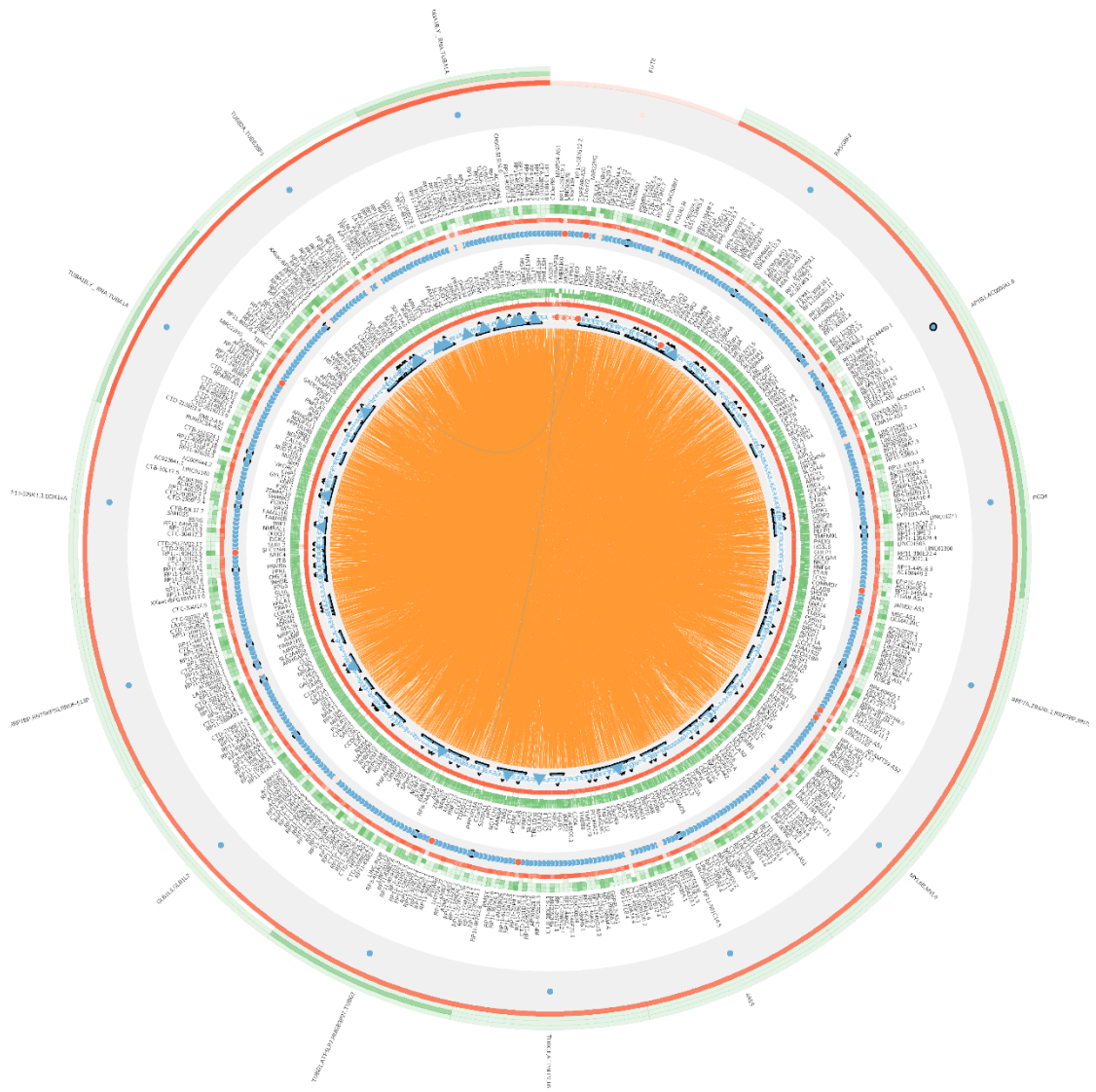


Figure S10. The module of ESC-specific genes, lncRNAs and circRNAs. There are three layers, the inner is the genes, the medium is the lncRNAs and the outside is circRNAs. There are two types of links, the orange is positive correlation and the blue represents negative correlation. Here, we used the symbol of host gene as the symbol of circRNA.

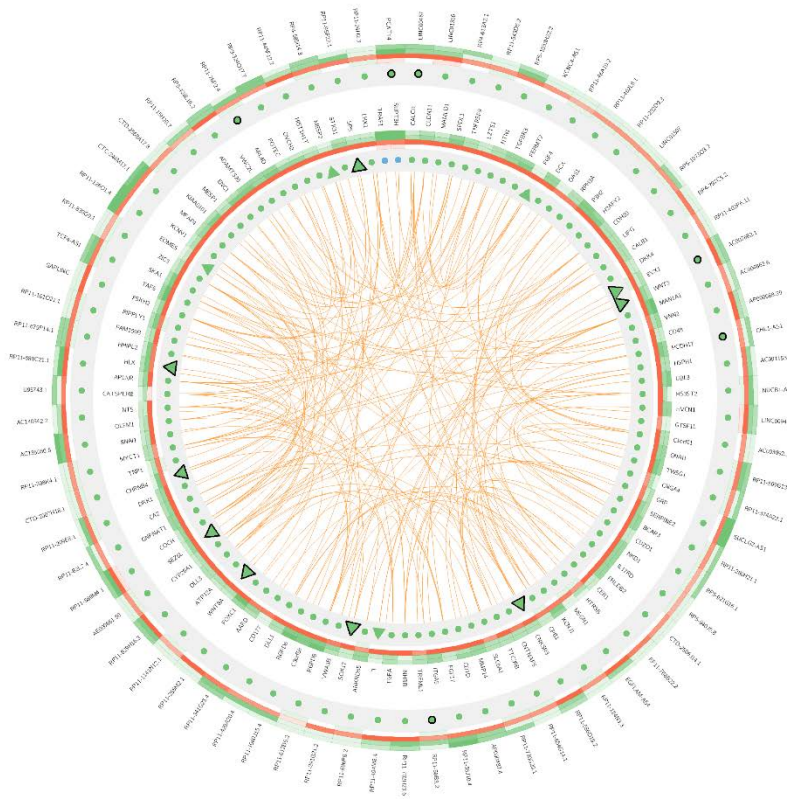


Figure S11. The module of MES-specific genes and lncRNAs.

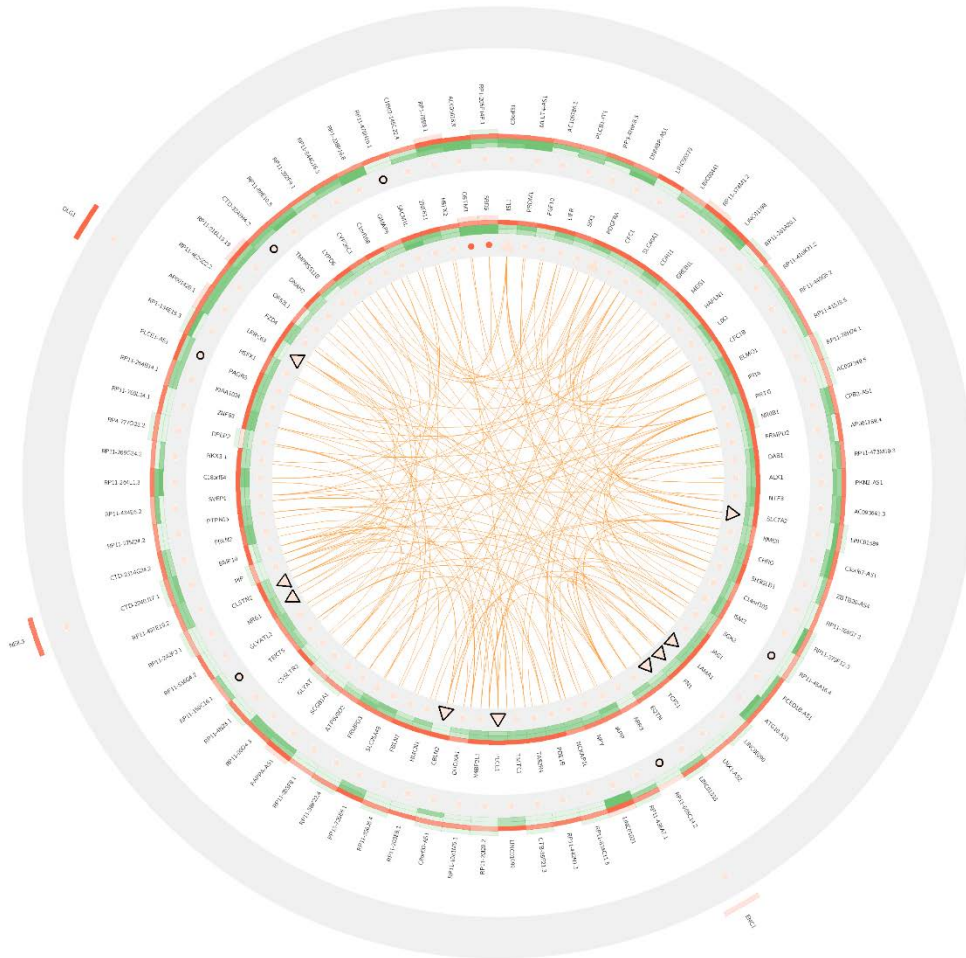


Figure S12. The module of CP-specific genes, lncRNAs and circRNAs.

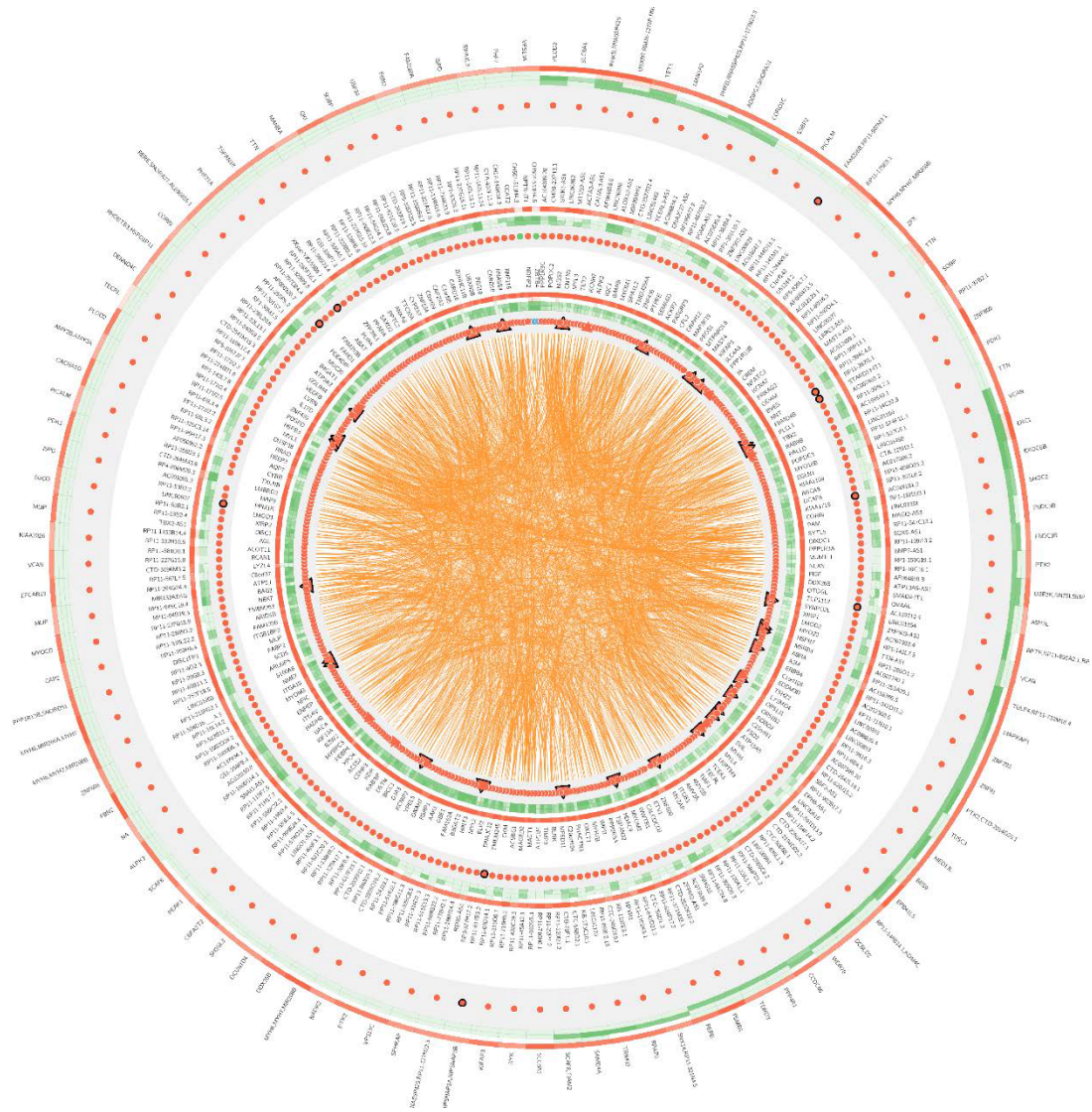


Figure S13. The module of CM-specific genes, lncRNAs and circRNAs.

Supplemental tables

Table S1. The gene expression patterns during heart differentiation. (Table S1.xlsx)

Table S2. The lncRNA expression patterns during heart differentiation. (Table S2.xlsx)

Table S3. The circRNA expression patterns during heart differentiation. (Table S3.xlsx)

Table S4. The network modules for the specific stage of heart differentiation. (Table S4.xlsx)

Table S5. Literature curation of the genes, lncRNAs and circRNAs in network modules. (Table S5.xlsx)